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<110> Holthofer, Harry
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<120> The Use of Soluble Protein Molecules Expressed by the Pancreas and Kidney Glomerulus

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<130> sequence
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<150> FI991369

<151> 1999-06-15

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<222> (1056)..(1093)

<213> Homo sapiens

<223> Transmembraneous domain

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Val Glu Leu Arg Cys Gly Val Ser Thr Pro Gly Ser Ala Val Gln Trp
50 55 60

Ala Lys Asp Gly Leu Leu Gly Pro Asp Pro Arg Ile Pro Gly Phe 65 70 75 80

Pro Arg Tyr Arg Leu Glu Gly Asp Pro Ala Arg Gly Glu Phe His Leu 85 90 95

Leu Ile Glu Ala Cys Asp Leu Ser Asp Asp Aia Glu Tyr Glu Cys Gln
100 105 110

Val Gly Arg Ser Glu Met Gly Pro Glu Leu Val Ser Pro Arg Val Ile 115 120 125

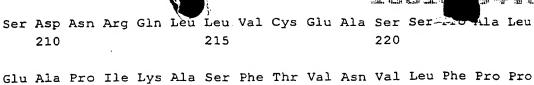
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Gly Thr Met Val Thr Trp Val Ala Gly Gln Glu Tyr Val Val Asn Cys 145 150 155 . 160

Val Ser Gly Asp Ala Lys Pro Ala Pro Asp Ile Thr Ile Leu Leu Ser 165 170 175

Gly Gln Thr Ile Ser Asp Ile Ser Ala Asn Val Asn Glu Gly Ser Gln 180 185 190

Gln Lys Leu Phe Thr Val Glu Ala Thr Ala Arg Val Thr Pro Arg Ser 195 200 205



Gly Pro Pro Val Ile Glu Trp Pro Gly Leu Asp Glu Gly His Val Arg 245 250 255

230

235

Ala Gly Gln Ser Leu Glu Leu Pro Cys Val Ala Arg Gly Gly Asn Pro 260 265 270

Ile Ala Thr Leu Gln Trp Leu Lys Asn Gly Gln Pro Val Ser Thr Ala 275 280 285

Trp Gly Thr Glu His Thr Gln Ala Val Ala Arg Ser Val Leu Val Met 290 295 300

Thr Val Arg Pro Glu Asp His Gly Ala Gln Leu Ser Cys Glu Ala His 305 310 315 320

Asn Ser Val Ser Ala Gly Thr Gln Glu His Gly Ile Thr Leu Gln Val 325 330 335

Thr Phe Pro Pro Ser Ala Ile Ile Ile Leu Gly Ser Ala Ser Gln Thr 340 345 350

Glu Asn Lys Asn Val Thr Leu Ser Cys Val Ser Lys Ser Ser Arg Pro 355 360 365

Arg Val Leu Leu Arg Trp Trp Leu Gly Trp Arg Gln Leu Leu Pro Met 370 375 380

Glu Glu Thr Val Met Asp Gly Leu His Gly Gly His Ile Ser Met Ser 385 390 395 400

Asn Leu Thr Phe Leu Ala Arg Arg Glu Asp Asn Gly Leu Thr Leu Thr 405 410 415

Cys Glu Ala Phe Ser Glu Ala Phe Thr Lys Glu Thr Phe Lys Lys Ser 420 425 430

Leu Ile Leu Asn Val Lys Tyr Pro Ala Gln Lys Leu Trp Ile Glu Gly . 435 440 445

Pro Pro Glu Gly Gln Lys Leu Arg Ala Gly Thr Arg Val Arg Leu Val 450 455 460

Cys	Leu Ala	Ile	Gly	Gry	Asn	Pro	Glu	Pro	Ser	Leu	Met	Trp-Tyr	Lys
465				470					475				480

Asp Ser Arg Thr Val Thr Glu Ser Arg Leu Pro Gln Glu Ser Arg Arg 485 490 495

Val His Leu Gly Ser Val Glu Lys Ser Gly Ser Thr Phe Ser Arg Glu 500 505 510

Leu Val Leu Val Thr Gly Pro Ser Asp Asn Gln Ala Lys Phe Thr Cys
515 520 525

Lys Ala Gly Gln Leu Ser Ala Ser Thr Gln Leu Ala Val Gln Phe Pro 530 540

Pro Thr Asn Val Thr Ile Leu Ala Asn Ala Ser Ala Leu Arg Pro Gly 545 550 555 560

Asp Ala Leu Asn Leu Thr Cys Val Ser Val Ser Ser Asn Pro Pro Val 565 570 575

Asn Leu Ser Trp Asp Lys Glu Gly Glu Arg Leu Glu Gly Val Ala Ala 580 585 590

Pro Pro Arg Arg Ala Pro Phe Lys Gly Ser Ala Ala Ala Arg Ser Val 595 600 605

Leu Leu Gln Val Ser Ser Arg Asp His Gly Gln Arg Val Thr Cys Arg 610 620

Ala His Ser Ala Glu Leu Arg Glu Thr Val Ser Ser Phe Tyr Arg Leu 625 630 635 640

Asn Val Leu Tyr Arg Pro Glu Phe Leu Gly Glu Gln Val Leu Val Val 645 650 655

Thr Ala Val Glu Gln Gly Glu Ala Leu Leu Pro Val Ser Val Ser Ala 660 665 670

Asn Pro Ala Pro Glu Ala Phe Asn Trp Thr Phe Arg Gly Tyr Arg Leu 675 680 685

Ser Pro Ala Gly Gly Pro Arg His Arg Ile Leu Ser Ser Gly Ala Leu 690 695 700

His Leu Trp Asn Val Thr Arg Ala Asp Asp Gly Leu Tyr Gln Leu His 705 710 715 720

- Cys Gln Asn Ser Glu Gly Thr Ala Glu Ala Arg Leu Arg Deu Asp Val
 725 730 735
- His Tyr Ala Pro Thr Ile Arg Ala Leu Gln Asp Pro Thr Glu Val Asn 740 745 750
- Val Gly Gly Ser Val Asp Ile Val Cys Thr Val Asp Ala Asn Pro Ile
 755 760 765
- Leu Pro Gly Met Phe Asn Trp Glu Arg Leu Gly Glu Asp Glu Glu Asp
 770 780
- Gln Ser Leu Asp Asp Met Glu Lys Ile Ser Arg Gly Pro Thr Gly Arg 785 790 795 800
- Leu Arg Ile His His Ala Lys Leu Ala Gln Ala Gly Ala Tyr Gln Cys 805 810 815
- Ile Val Asp Asn Gly Val Ala Pro Pro Ala Arg Arg Leu Leu Arg Leu 820 825 830
- Val Val Arg Phe Ala Pro Gln Val Glu His Pro Thr Pro Leu Thr Lys 835 840 845
- Val Ala Ala Ala Gly Asp Ser Thr Ser Ser Ala Thr Leu His Cys Arg 850 855 860
- Ala Arg Gly Val Pro Asn Ile Val Phe Thr Trp Thr Lys Asn Gly Val 865 870 875 880
- Pro Leu Asp Leu Gln Asp Pro Arg Tyr Thr Glu His Thr Tyr His Gln 885 890 895
- Gly Gly Val His Ser Ser Leu Leu Thr Ile Ala Asn Val Ser Ala Ala 900 905 910
- Gln Asp Tyr Ala Leu Phe Thr Cys Thr Ala Thr Asn Ala Leu Gly Ser 915 920 925
- Asp Gln Thr Asn Ile Gln Leu Val Ser Ile Ser Arg Pro Asp Pro Pro 930 935 940
- Ser Gly Leu Lys Val Val Ser Leu Thr Pro His Ser Val Gly Leu Glu 945 950 955 960
- Trp Lys Pro Gly Phe Asp Gly Gly Leu Pro Gln Arg Phe Cys Ile Arg 965 970 975

Tyr Glu Ala Leu Gly Pro Gly Phe His Tyr Val Asp Val Pro 980 985 990

- Pro Gln Ala Thr Thr Phe Thr Leu Thr Gly Leu Gln Pro Ser Thr Arg
 995 1000 1005
- Tyr Arg Val Trp Leu Leu Ala Ser Asn Ala Leu Gly Asp Ser Gly Leu 1010 1015 1020
- Ala Asp Lys Gly Thr Gln Leu Pro Ile Thr Thr Pro Gly Leu His Gln 1025 1030 1035 1040
- Pro Ser Gly Glu Pro Glu Asp Gln Leu Pro Thr Glu Pro Pro Ser Gly
 . 1045 1050 1055
- Pro Ser Gly Leu Pro Leu Leu Pro Val Leu Phe Ala Leu Gly Gly Leu 1060 1065 1070
- Leu Leu Ser Asn Ala Ser Cys Val Gly Gly Val Leu Trp Gln Arg 1075 1080 1085
- Arg Leu Arg Arg Leu Ala Glu Gly Ile Ser Glu Lys Thr Glu Ala Gly 1090 1095 1100
- Ser Glu Glu Asp Arg Val Arg Asn Glu Tyr Glu Glu Ser Gln Trp Thr 1105 1110 1115 1120
- Gly Glu Arg Asp Thr Gln Ser Ser Thr Val Ser Thr Thr Glu Ala Glu 1125 1130 1135
- Pro Tyr Tyr Arg Ser Leu Arg Asp Phe Ser Pro Gln Leu Pro Pro Thr 1140 1145 1150
- Gln Glu Glu Val Ser Tyr Ser Arg Gly Phe Thr Gly Glu Asp Glu Asp 1155 1160 1165
- Met Ala Phe Pro Gly His Leu Tyr Asp Glu Val Glu Arg Thr Tyr Pro 1170 1175 1180
- Pro Ser Gly Ala Trp Gly Pro Leu Tyr Asp Glu Val Gln Met Gly Pro 1185 1190 1195 1200
- Trp Asp Leu His Trp Pro Glu Asp Thr Tyr Gln Asp Pro Arg Gly Ile 1205 1210 1215
- Tyr Asp Gln Val Ala Gly Asp Leu Asp Thr Leu Glu Pro Asp Ser Leu
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Pro Phe Glu Leu Arg Gry His Leu Val 1235 . 1240

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<213> Homo sapiens

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<213> Homo sapiens

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<222> (1)..(13)

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<213> Artificial Sequence

WO 00/77044





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